



wwPDB EM Validation Summary Report ⓘ

Mar 22, 2026 – 02:58 PM UTC

PDB ID : 8ATU / pdb_00008atu
EMDB ID : EMD-15663
Title : Cryo-EM structure of human BIRC6
Authors : Ehrmann, J.F.; Grabarczyk, D.B.; Clausen, T.
Deposited on : 2022-08-24
Resolution : 3.30 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

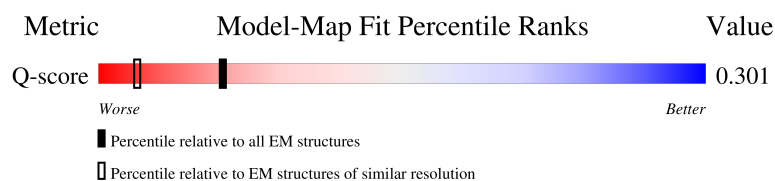
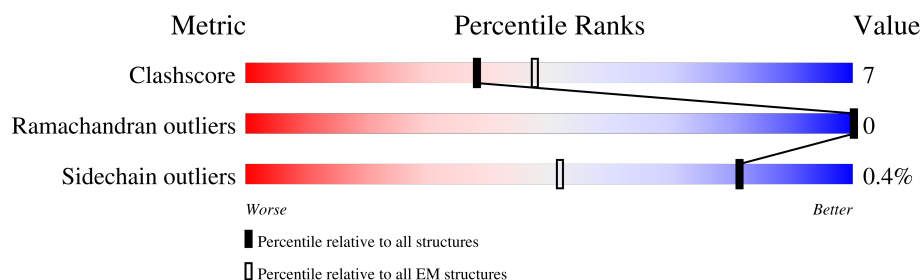
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15087 (2.80 - 3.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	4867	34% 47% 11% 42%
1	B	4867	34% 47% 11% 42%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 43882 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Baculoviral IAP repeat-containing protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2837	Total	C	N	O	S	0	0
			21940	14019	3711	4059	151		
1	B	2837	Total	C	N	O	S	0	0
			21940	14019	3711	4059	151		

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1332	VAL	LEU	conflict	UNP Q9NR09
A	4858	SER	-	expression tag	UNP Q9NR09
A	4859	ALA	-	expression tag	UNP Q9NR09
A	4860	TRP	-	expression tag	UNP Q9NR09
A	4861	SER	-	expression tag	UNP Q9NR09
A	4862	HIS	-	expression tag	UNP Q9NR09
A	4863	PRO	-	expression tag	UNP Q9NR09
A	4864	GLN	-	expression tag	UNP Q9NR09
A	4865	PHE	-	expression tag	UNP Q9NR09
A	4866	GLU	-	expression tag	UNP Q9NR09
A	4867	LYS	-	expression tag	UNP Q9NR09
B	1332	VAL	LEU	conflict	UNP Q9NR09
B	4858	SER	-	expression tag	UNP Q9NR09
B	4859	ALA	-	expression tag	UNP Q9NR09
B	4860	TRP	-	expression tag	UNP Q9NR09
B	4861	SER	-	expression tag	UNP Q9NR09
B	4862	HIS	-	expression tag	UNP Q9NR09
B	4863	PRO	-	expression tag	UNP Q9NR09
B	4864	GLN	-	expression tag	UNP Q9NR09
B	4865	PHE	-	expression tag	UNP Q9NR09
B	4866	GLU	-	expression tag	UNP Q9NR09
B	4867	LYS	-	expression tag	UNP Q9NR09

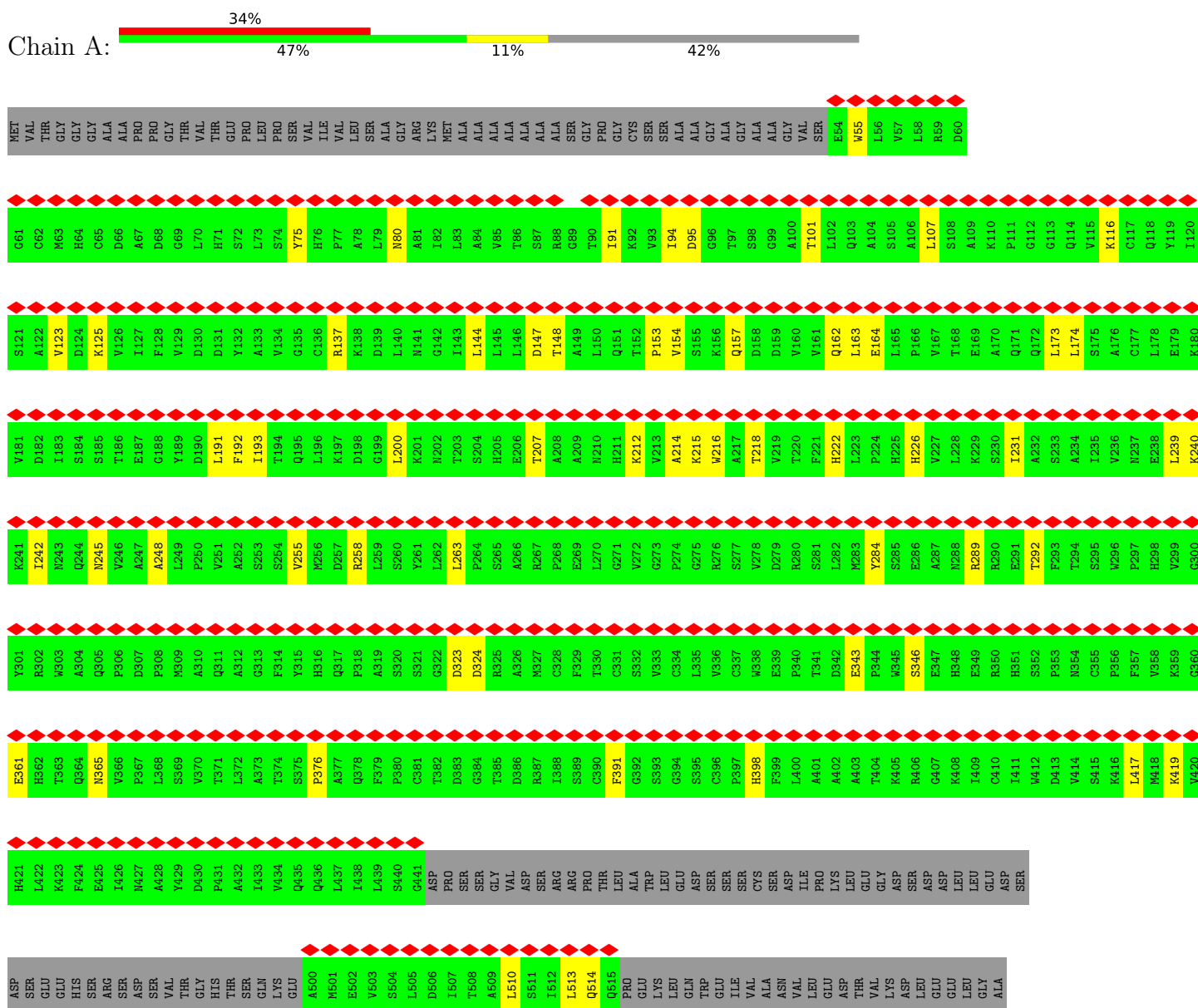
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total 1	Zn 1	0
2	B	1	Total 1	Zn 1	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Baculoviral IAP repeat-containing protein 6





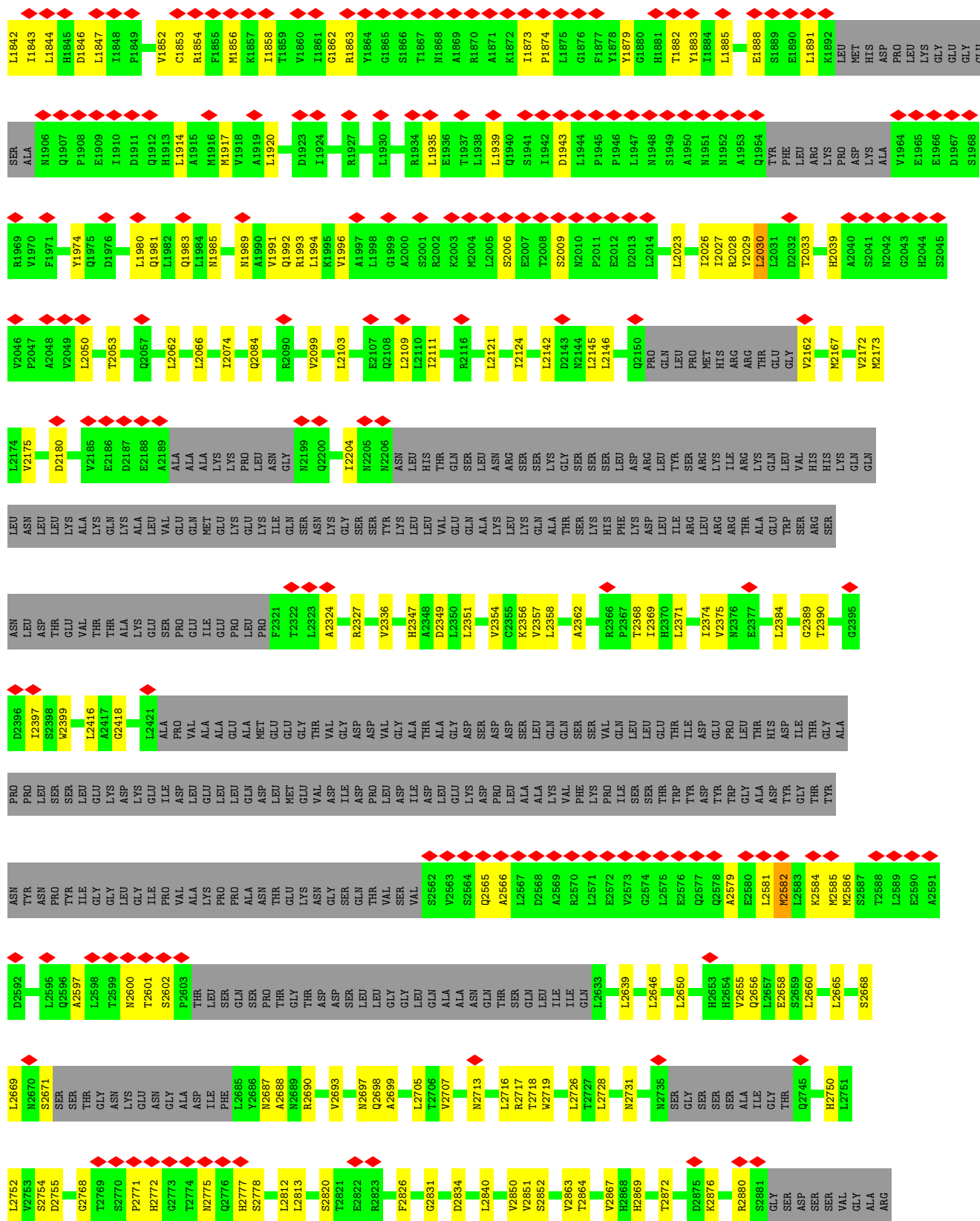
VAL	HIS	GLY	V2162	HIS	S2041	GLY	H1840	I1780	VAL	THR	SER	V1537	D1460	R1382	L1322
HIS	GLY	HIS	V2162	HIS	S2041	GLY	S1841	E1781	ILE	ALA	GLY	L1538	E1461	K1383	Q1323
LYS	GLN	LYS	M2167	GLN	G2043	SER	L1842	R1782	ASN	ALA	VAL	GLY	D1462	F1384	F1324
GLN	GLN	GLN	M2173	GLN	H2044	ALA	L1843	M1783	GLU	ALA	ALA	GLY	GLY	L1385	S1325
LEU	LEU	LEU	M2174	LEU	S2045	ALA	L1844	H1784	LEU	ALA	ALA	GLY	GLY	S1386	E1326
ASN	ASN	ASN	L2174	ASN	V2046	ALA	H1845	S1785	GLN	ALA	ALA	LYS	D1387	F1327	F1327
LEU	LEU	LEU	V2175	LEU	P2047	ALA	D1846	G1786	VAL	ALA	THR	VAL	L1473	H1328	H1328
ALA	ALA	ALA	D2180	ALA	V2049	ALA	L1847	A1787	PRO	ALA	SER	SER	L1474	E1329	E1329
LYS	LYS	LYS	V2185	LYS	L2050	ALA	P1849	R1789	GLY	GLY	THR	CYS	V1477	K1330	K1330
GLN	GLN	GLN	E2186	GLN	L2053	ALA	V1852	F1790	VAL	VAL	ALA	ALA	S1478	L1331	L1331
LYS	LYS	LYS	D2187	LYS	L1980	ALA	C1853	V1791	ILE	HIS	ALA	ALA	R1479	V1332	V1332
ALA	ALA	ALA	E2188	ALA	Q1981	ALA	R1854	T1792	ASP	SER	VAL	GLN	E1396	G1397	G1397
VAL	VAL	VAL	A2189	VAL	L1982	ALA	F1855	L1793	PRO	SER	VAL	ALA	R1398	R1398	T1334
GLY	GLY	GLY	ALA	GLY	M1917	ALA	M1856	D1794	ALA	PRO	LEU	LEU	I1400	L1335	L1335
ALA	ALA	ALA	ALA	ALA	M1918	ALA	K1857	F1795	VAL	SER	GLN	GLN	T1486	C1336	C1336
MET	MET	MET	ALA	MET	L1920	ALA	I1858	G1796	ASN	ASN	SER	SER	E1489	R1337	R1337
GLY	GLY	GLY	ALA	GLY	D1923	ALA	T1859	R1797	LEU	PRO	LEU	LEU	A1405	K1338	K1338
LYS	LYS	LYS	ALA	LYS	I1924	ALA	V1860	P1798	ALA	VAL	SER	SER	A1406	T1339	T1339
PRO	PRO	PRO	ALA	PRO	I1924	ALA	I1861	I1799	ALA	ALA	HIS	HIS	L1491	D1340	D1340
LYS	LYS	LYS	ALA	LYS	R1927	ALA	G1862	L1800	ASN	ALA	ALA	ALA	Q1493	G1342	G1342
ASN	ASN	ASN	ALA	ASN	L1930	ALA	R1863	L1801	LYS	GLY	ALA	ALA	T1494	Q1343	Q1343
GLY	GLY	GLY	ALA	GLY	R1934	ALA	I1864	L1802	SER	PHE	PHE	GLU	R1495	I1344	I1344
LYS	LYS	LYS	ALA	LYS	L1934	ALA	G1865	D1803	ASN	ILE	ALA	ALA	L1498	T1345	T1345
GLY	GLY	GLY	ALA	GLY	R1934	ALA	S1866	V1804	LYS	HIS	GLN	GLN	E1346	E1346	E1346
SER	SER	SER	ALA	SER	L1934	ALA	T1867	I1805	SER	PRO	GLN	GLN	D1504	H1347	H1347
TYR	TYR	TYR	ALA	TYR	L1935	ALA	I1806	I1806	ARG	SER	LEU	LEU	P1505	A1348	A1348
LYS	LYS	LYS	ALA	LYS	E1936	ALA	M1868	P1807	MET	ASP	VAL	VAL	K1416	Q1349	Q1349
LEU	LEU	LEU	ALA	LEU	L1937	ALA	A1869	T1808	ASN	ASN	GLN	GLN	C1417	S1350	S1350
LEU	LEU	LEU	ALA	LEU	L1938	ALA	R1870	G1810	PRO	ILE	LEU	LEU	L1510	L1351	L1351
VAL	VAL	VAL	ALA	VAL	L1939	ALA	A1871	D1811	GLY	PRO	GLU	GLU	E1511	V1352	V1352
GLN	GLN	GLN	ALA	GLN	Q1940	ALA	K1872	L1812	SER	THR	THR	THR	S1513	L1353	L1353
LYS	LYS	LYS	ALA	LYS	S1941	ALA	I1873	D1813	THR	LYS	LYS	LYS	G1514	D1354	D1354
LEU	LEU	LEU	ALA	LEU	I1942	ALA	P1874	L1814	THR	THR	LEU	LEU	S1515	T1355	T1355
ARG	ARG	ARG	ALA	ARG	D1943	ALA	L1875	S1814	PRO	PRO	LEU	LEU	A1423	L1356	L1356
SER	SER	SER	ALA	SER	L1944	ALA	G1876	L1815	LEU	LEU	LYS	LYS	F1424	C1357	C1357
ALA	ALA	ALA	ALA	ALA	P1946	ALA	F1877	S1816	PHE	PHE	LEU	LEU	G1426	V1358	V1358
THR	THR	THR	ALA	THR	L1947	ALA	Y1878	I1817	THR	THR	GLN	GLN	P1427	L1359	L1359
LYS	LYS	LYS	ALA	LYS	L1948	ALA	G1880	I1819	THR	THR	GLN	GLN	V1427	A1360	A1360
HIS	HIS	HIS	ALA	HIS	L1949	ALA	H1881	V1820	PRO	PRO	LYS	LYS	L1428	G1361	G1361
PHE	PHE	PHE	ALA	PHE	A1950	ALA	T1882	T1821	ALA	LEU	ALA	ALA	L1429	V1362	V1362
ASP	ASP	ASP	ALA	ASP	N1951	ALA	I1883	G1823	THR	THR	LYS	LYS	K1430	H1363	H1363
LEU	LEU	LEU	ALA	LEU	N1952	ALA	L1884	L1824	PRO	PRO	LEU	LEU	A1431	S1364	S1364
LEU	LEU	LEU	ALA	LEU	A1953	ALA	L1885	E1824	ASN	ASN	ALA	ALA	L1432	N1365	N1365
ILE	ILE	ILE	ALA	ILE	Q1954	ALA	E1888	E1825	VAL	VAL	GLY	GLY	L1433	G1366	G1366
THR	THR	THR	ALA	THR	TYR	ALA	S1889	V1826	GLY	GLY	THR	THR	L1439	P1367	P1367
ARG	ARG	ARG	ALA	ARG	LEU	ALA	E1890	D1827	THR	THR	VAL	VAL	P1440	G1368	G1368
ARG	ARG	ARG	ALA	ARG	ARG	ALA	L1891	G1828	GLY	GLY	GLN	GLN	A1441	S1369	S1369
LYS	LYS	LYS	ALA	LYS	LYS	ALA	K1892	R1829	ALA	ALA	ALA	ALA	G1445	S1370	S1370
GLN	GLN	GLN	ALA	GLN	PRO	ALA	LEU	R1830	THR	THR	THR	THR	F1452	K1371	K1371
LEU	LEU	LEU	ALA	LEU	ASP	ALA	MET	L1831	VAL	VAL	GLY	GLY	N1456	G1373	G1373
THR	THR	THR	ALA	THR	LYS	ALA	HIS	V1832	THR	THR	THR	THR	Y1457	N1374	N1374
					V1964	ALA	ASP	V1833	SER	SER	GLN	GLN	V1458	E1375	E1375
					E1965	ALA	PRO	A1834	THR	THR	GLY	GLY	K1459	N1376	N1376
					E1966	ALA	LEU	T1835	VAL	VAL	LEU	LEU		L1377	L1377
							LYS	D1836	GLY	GLY	GLY	GLY		E1379	E1379
							GLU	I1837	THR	THR	THR	THR		K1380	K1380
								S1838	THR	THR	THR	THR		T1381	T1381
								T1839	THR	THR	THR	THR			















LEU	MET	HIS	ASP	GLN	VAL	LYS	PRO	SER	SER	SER	LYS	GLU	LEU	PRO	SER	ASP	PHE	GLN	LEU	SER	ALA	TRP	SER	HIS	PRO	GLN	PHE	GLU	LYS
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	136799	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.066	Depositor
Minimum map value	-0.036	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.012	Depositor
Map size (Å)	425.87997, 425.87997, 425.87997	wwPDB
Map dimensions	364, 364, 364	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.17, 1.17, 1.17	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.15	0/22350	0.39	4/30362 (0.0%)
1	B	0.15	0/22350	0.39	4/30362 (0.0%)
All	All	0.15	0/44700	0.39	8/60724 (0.0%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1807	PRO	CA-N-CD	-12.75	94.15	112.00
1	B	1807	PRO	CA-N-CD	-12.74	94.16	112.00
1	B	1426	PRO	CA-N-CD	-9.63	98.52	112.00
1	A	1426	PRO	CA-N-CD	-9.60	98.56	112.00
1	B	2850	VAL	N-CA-C	-5.30	108.11	113.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	21940	0	22350	343	0
1	B	21940	0	22350	334	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	43882	0	44700	658	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 658 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3984:ALA:HB1	1:A:4067:ILE:H	1.52	0.74
1:B:3984:ALA:HB1	1:B:4067:ILE:H	1.51	0.72
1:A:3547:CYS:HG	1:A:3846:HIS:HE2	1.40	0.69
1:B:3547:CYS:HG	1:B:3846:HIS:HE2	1.41	0.68
1:A:2145:LEU:HD21	1:A:2167:MET:HG3	1.75	0.68

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2745/4867 (56%)	2649 (96%)	96 (4%)	0	100	100
1	B	2745/4867 (56%)	2650 (96%)	95 (4%)	0	100	100
All	All	5490/9734 (56%)	5299 (96%)	191 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	2497/4225 (59%)	2488 (100%)	9 (0%)	84	84
1	B	2497/4225 (59%)	2488 (100%)	9 (0%)	84	84
All	All	4994/8450 (59%)	4976 (100%)	18 (0%)	81	84

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	2582	MET
1	B	3690	LEU
1	B	3333	LEU
1	A	3690	LEU
1	B	2030	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1297	GLN
1	B	2205	ASN
1	B	4180	HIS
1	B	1343	GLN
1	B	1988	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

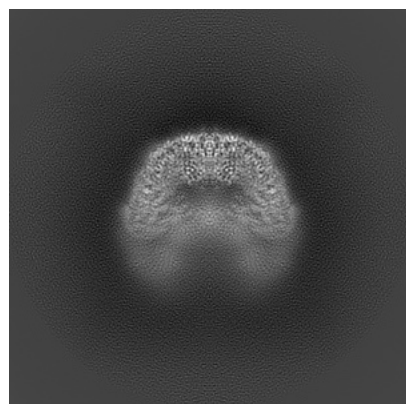
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15663. These allow visual inspection of the internal detail of the map and identification of artifacts.

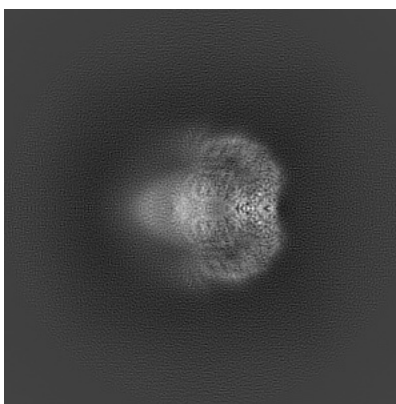
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

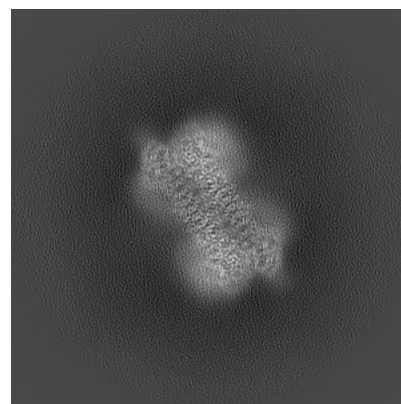
6.1.1 Primary map



X

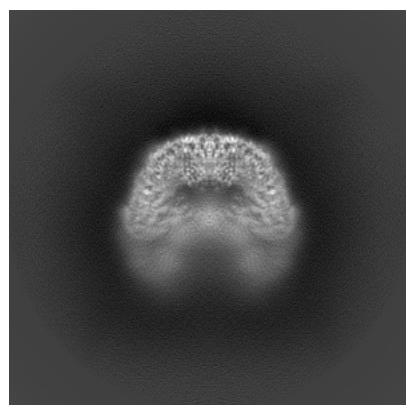


Y

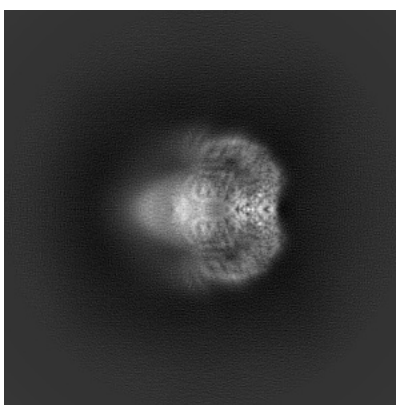


Z

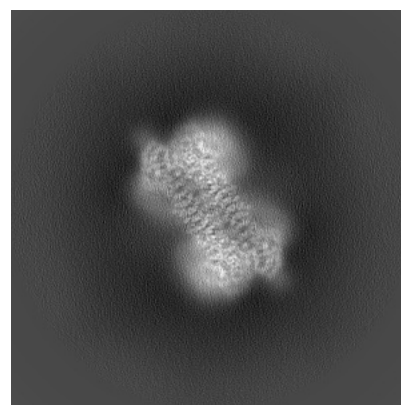
6.1.2 Raw map



X



Y

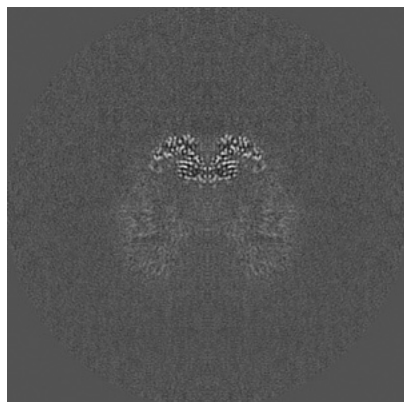


Z

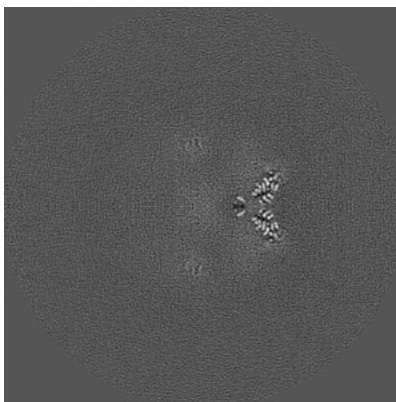
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

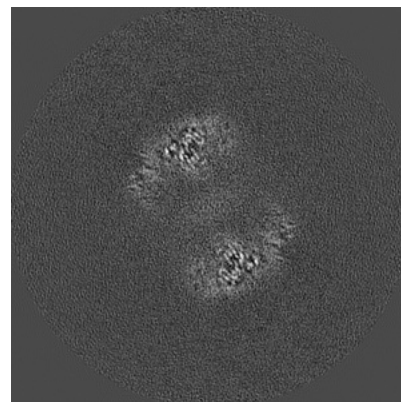
6.2.1 Primary map



X Index: 182

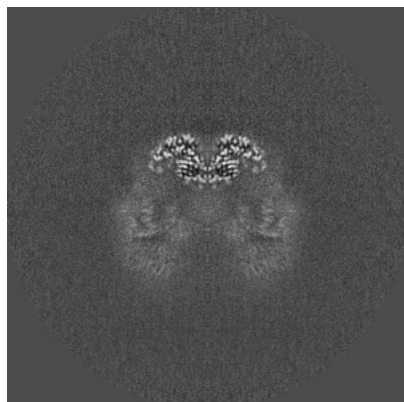


Y Index: 182

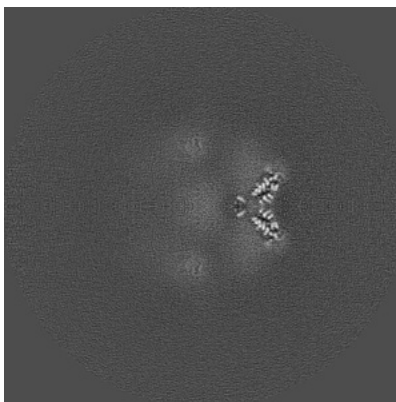


Z Index: 182

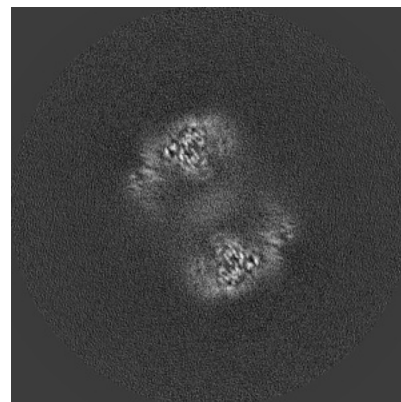
6.2.2 Raw map



X Index: 182



Y Index: 182

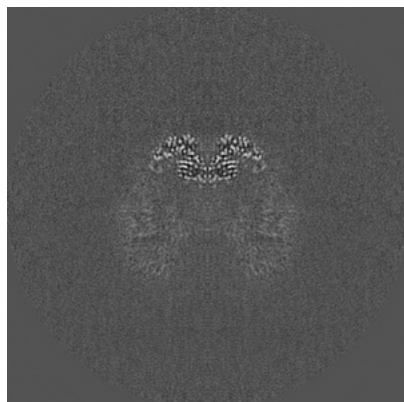


Z Index: 182

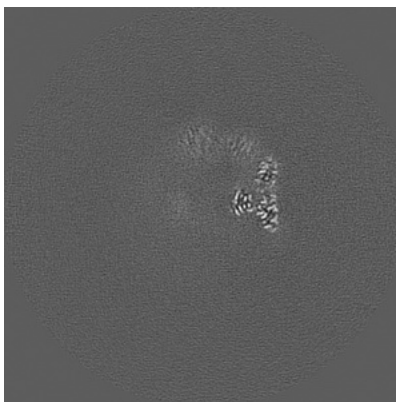
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

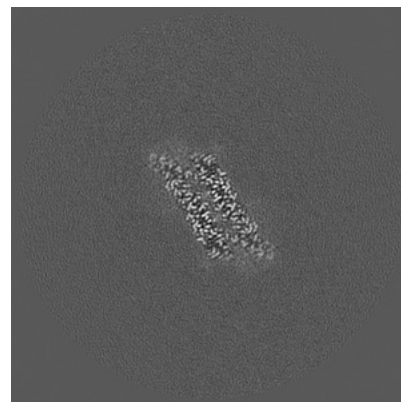
6.3.1 Primary map



X Index: 182

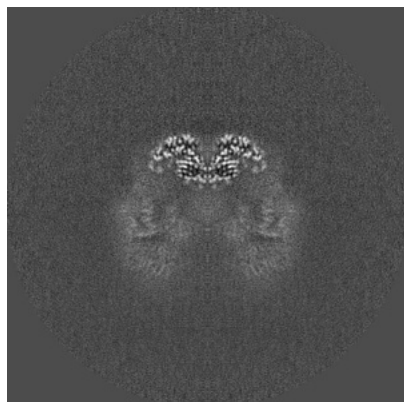


Y Index: 161

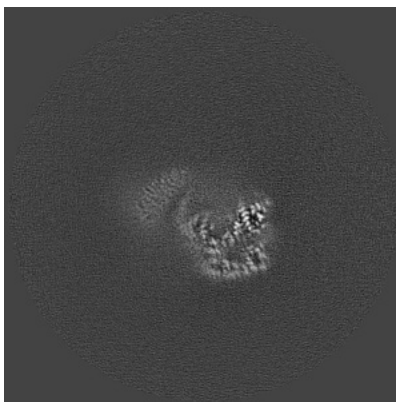


Z Index: 236

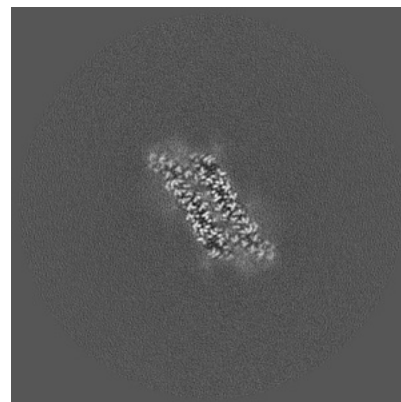
6.3.2 Raw map



X Index: 182



Y Index: 227

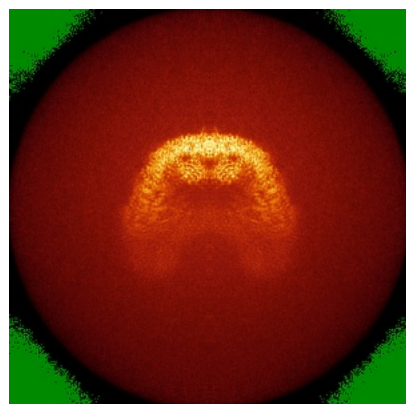


Z Index: 236

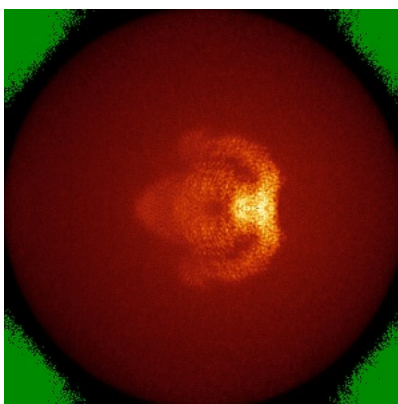
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

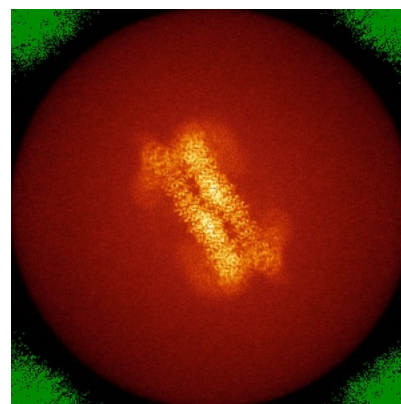
6.4.1 Primary map



X

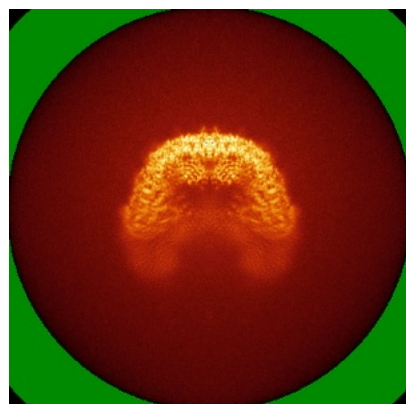


Y

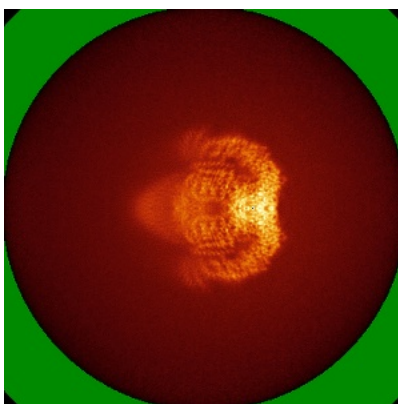


Z

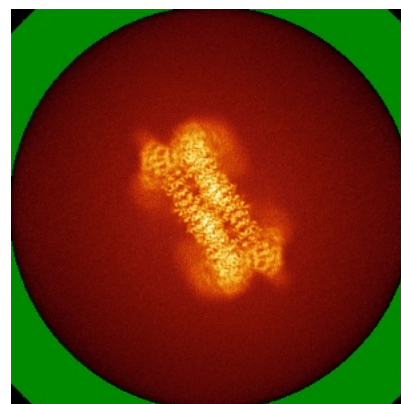
6.4.2 Raw map



X



Y



Z

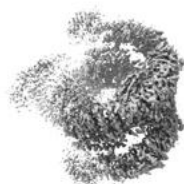
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



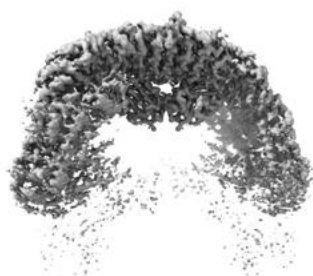
Y



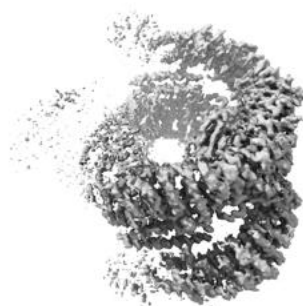
Z

The images above show the 3D surface view of the map at the recommended contour level 0.012. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

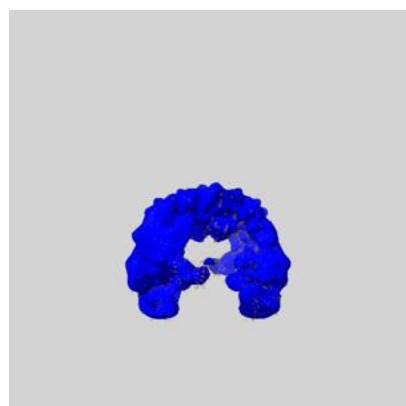
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

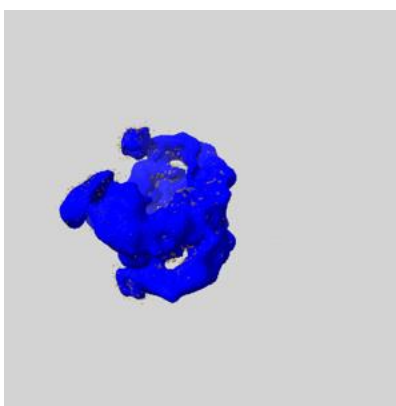
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

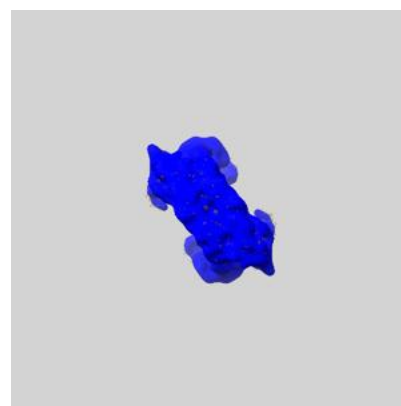
6.6.1 emd_15663_msk_1.map [i](#)



X



Y

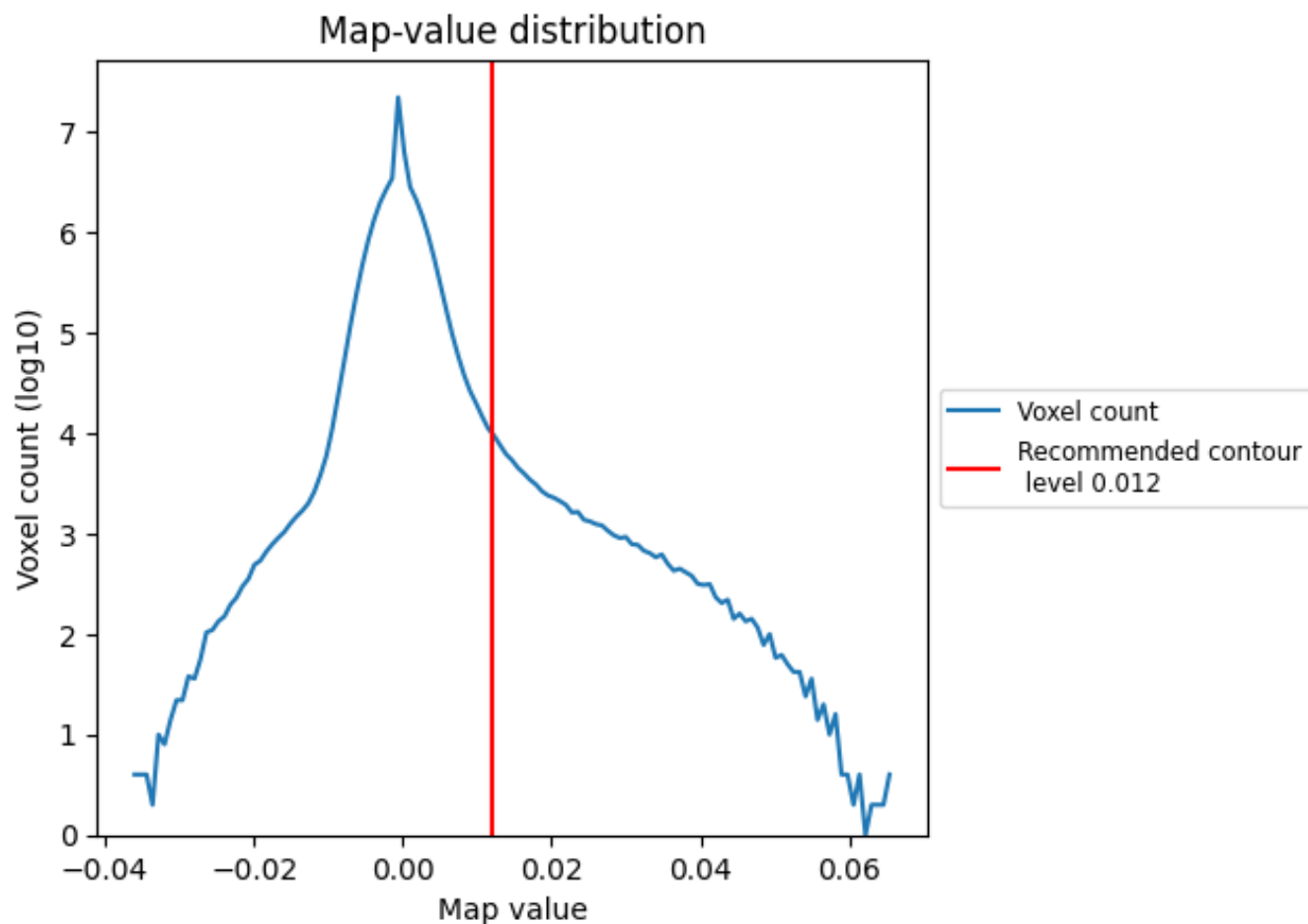


Z

7 Map analysis [i](#)

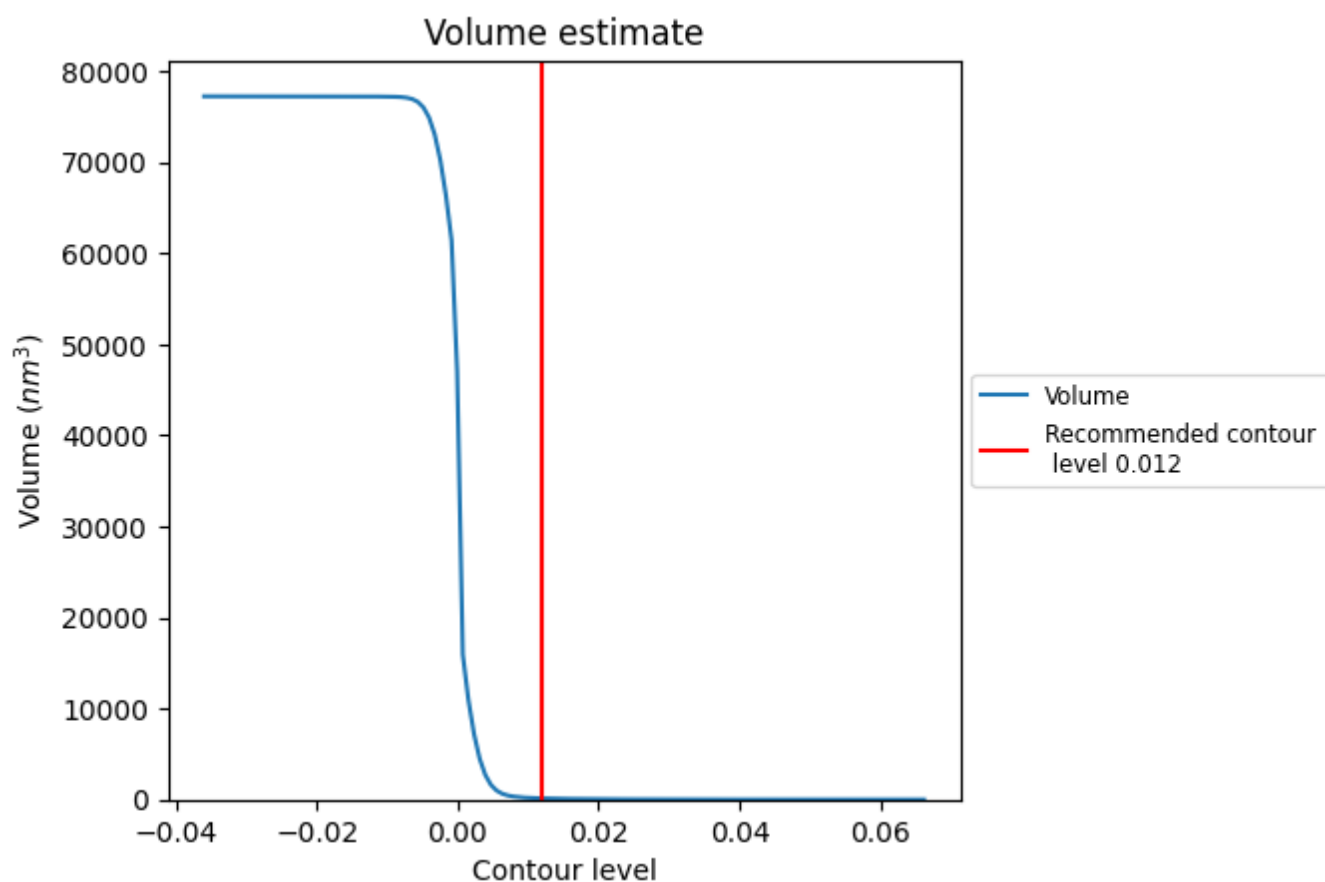
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

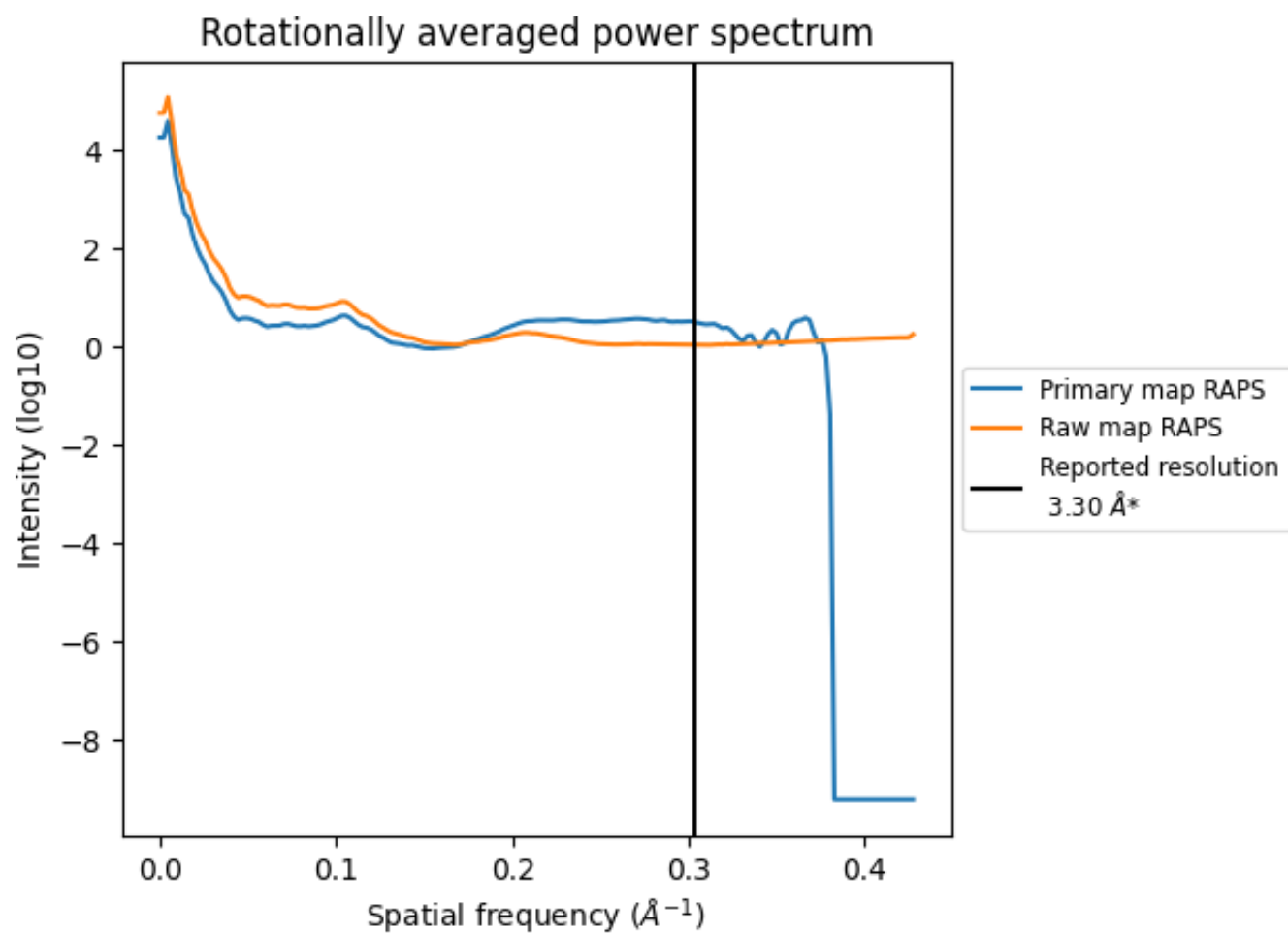
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 128 nm³; this corresponds to an approximate mass of 116 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

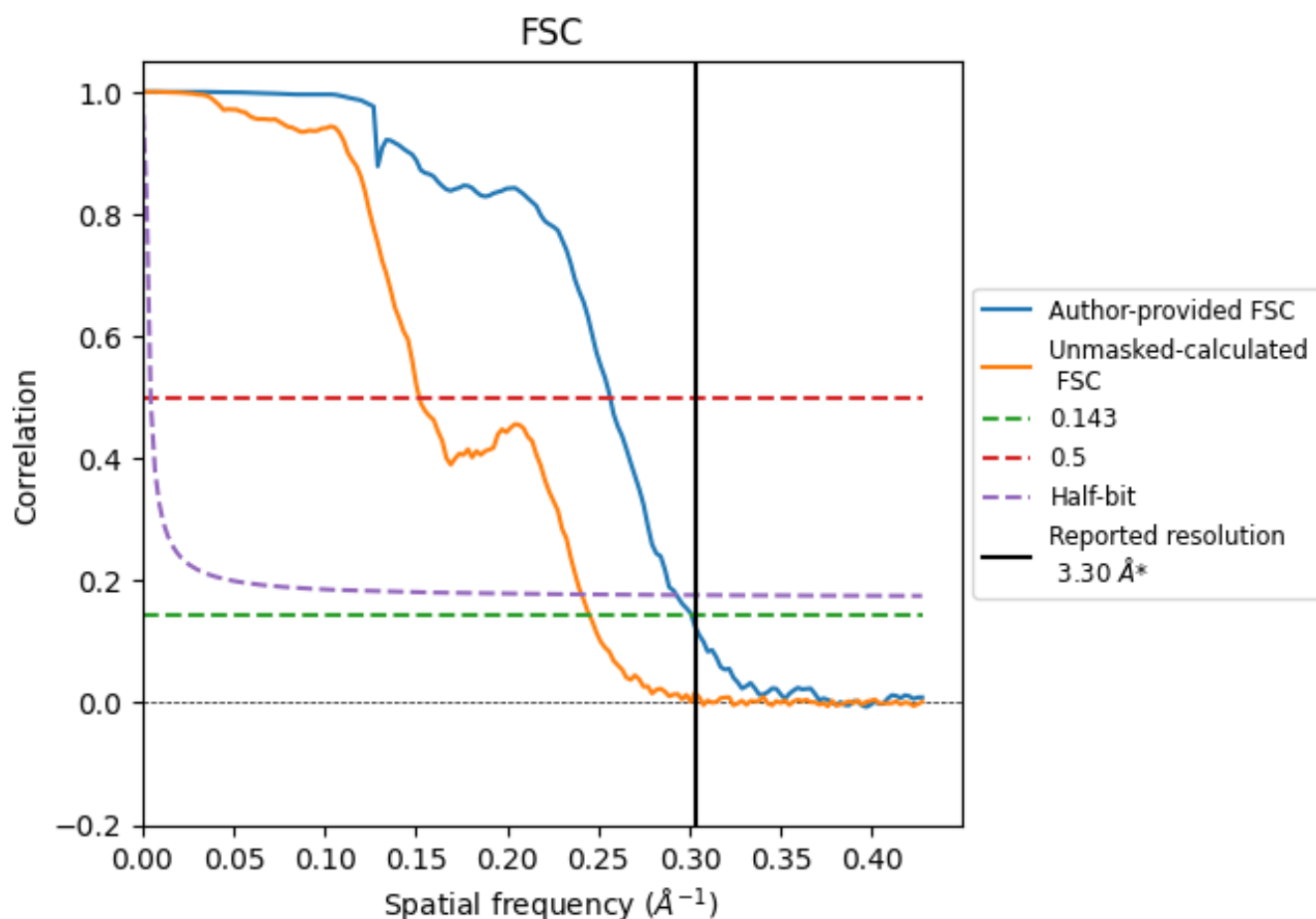


*Reported resolution corresponds to spatial frequency of 0.303 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

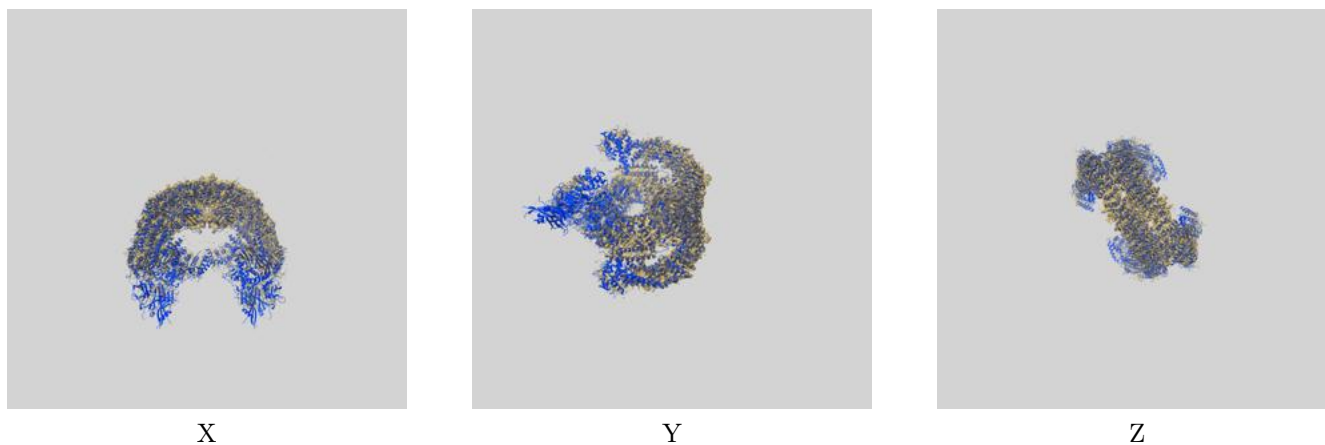
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.32	3.90	3.42
Unmasked-calculated*	4.08	6.59	4.15

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.08 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

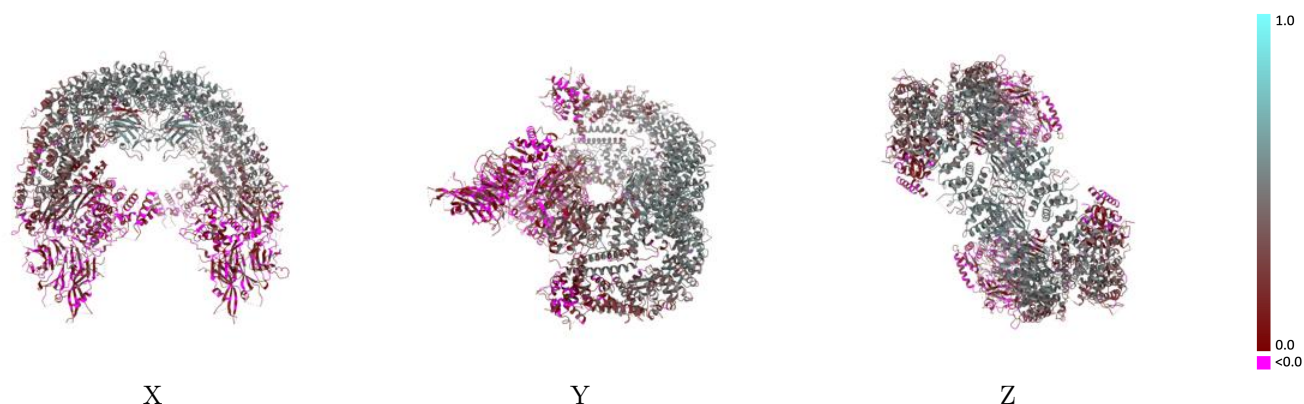
This section contains information regarding the fit between EMDB map EMD-15663 and PDB model 8ATU. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



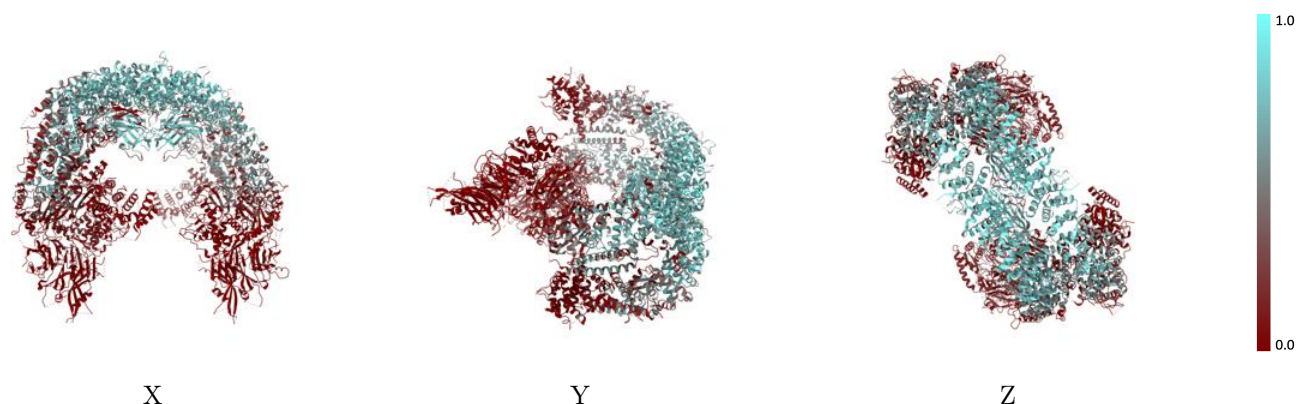
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



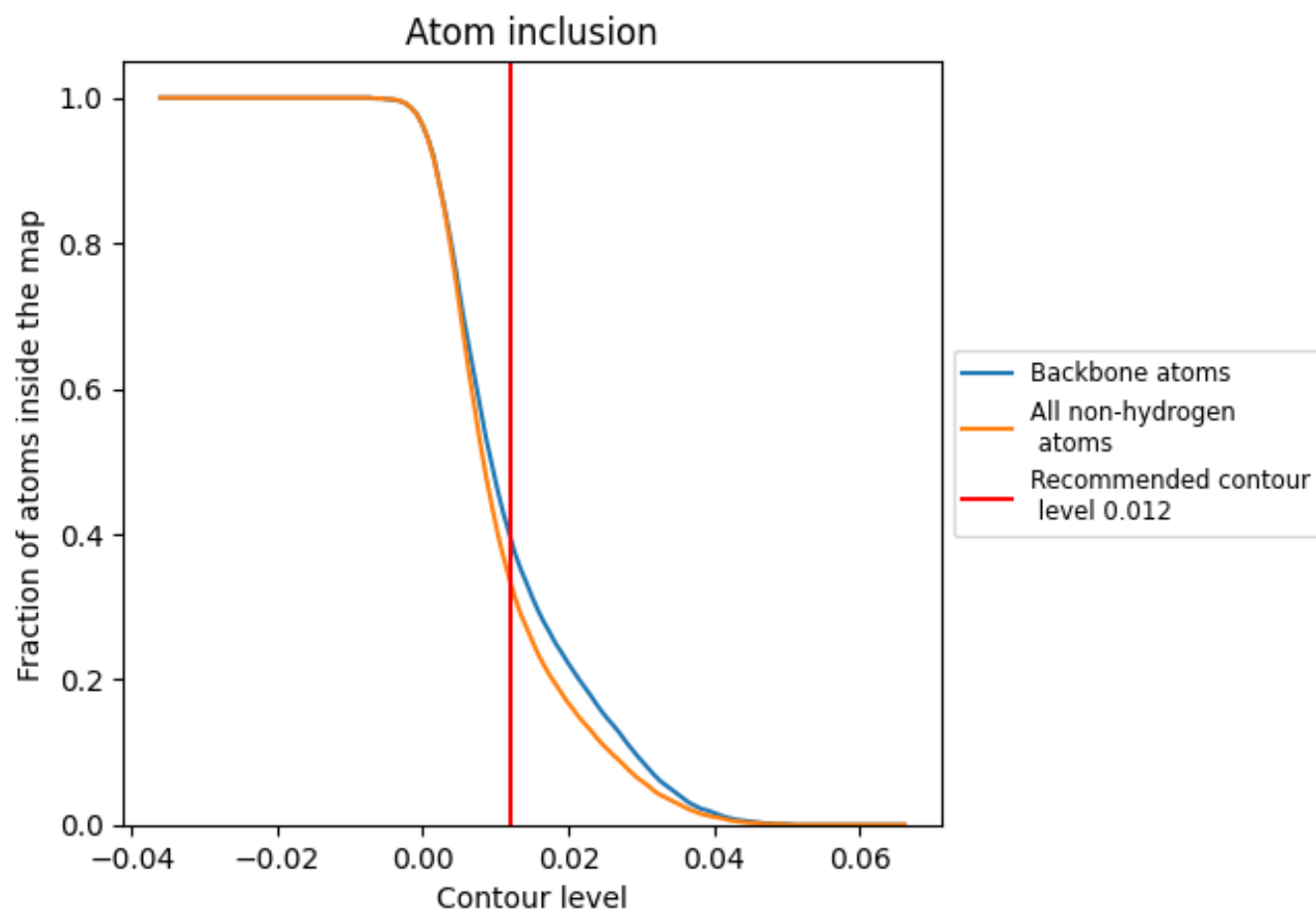
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.012).

9.4 Atom inclusion [i](#)



At the recommended contour level, 40% of all backbone atoms, 34% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3350	0.3010
A	0.3350	0.3010
B	0.3350	0.3010

